

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 16:53:39 ; Search time 156 Seconds
(without alignment)
230.757 Million cell updates/sec

Title: US-10-613-228A-1

Perfect score: 22

Sequence: 1 tcgcgttttcgtcgttttt 22

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCITS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------------------|--------------------|
| 1 | 17.2 | 78.2 | 133 | US-09-313-294A-108 | Sequence 108, App |
| 2 | 17.2 | 78.2 | 513 | US-09-107-532A-292 | Sequence 292, App |
| 3 | 16.8 | 76.4 | 36016 | US-09-949-016-14223 | Sequence 14223, A |
| 4 | 16.4 | 74.5 | 3531 | US-08-629-600-1 | Sequence 1, Appl |
| 5 | 16.4 | 74.5 | 3531 | US-09-076-761-1 | Sequence 1, Appl |
| 6 | 16.2 | 73.6 | 909 | US-09-134-000C-3167 | Sequence 3167, App |
| 7 | 16.2 | 73.6 | 2358 | US-09-134-000C-3285 | Sequence 3285, App |
| 8 | 15.8 | 71.8 | 660 | US-09-489-039A-560 | Sequence 560, App |
| 9 | 15.6 | 70.9 | 231 | US-09-543-681A-2772 | Sequence 2772, App |
| 10 | 15.6 | 70.9 | 300 | US-09-543-681A-1478 | Sequence 1478, App |
| 11 | 15.6 | 70.9 | 440 | US-09-513-999C-35185 | Sequence 35185, A |
| 12 | 15.6 | 70.9 | 599 | US-09-270-767-3552 | Sequence 3552, App |
| 13 | 15.6 | 70.9 | 599 | US-09-270-767-18834 | Sequence 18834, A |
| 14 | 15.6 | 70.9 | 601 | US-09-949-016-31352 | Sequence 31352, A |
| 15 | 15.6 | 70.9 | 601 | US-09-949-016-69221 | Sequence 69221, A |
| 16 | 15.6 | 70.9 | 601 | US-09-949-016-81370 | Sequence 81370, A |
| 17 | 15.6 | 70.9 | 601 | US-09-949-016-127420 | Sequence 127420, A |
| 18 | 15.6 | 70.9 | 601 | US-09-949-016-177125 | Sequence 177125, A |
| 19 | 15.6 | 70.9 | 601 | US-09-949-016-177126 | Sequence 177126, A |
| 20 | 15.6 | 70.9 | 601 | US-09-949-016-177127 | Sequence 177127, A |
| 21 | 15.6 | 70.9 | 678 | US-09-134-001C-2551 | Sequence 2551, App |
| 22 | 15.6 | 70.9 | 826 | US-09-221-017B-1008 | Sequence 1008, App |
| 23 | 15.6 | 70.9 | 850 | US-08-617-860B-34 | Sequence 34, Appl |
| 24 | 15.6 | 70.9 | 1068 | US-09-543-681A-2972 | Sequence 2972, App |
| 25 | 15.6 | 70.9 | 1734 | US-09-248-796A-4704 | Sequence 4704, App |
| 26 | 15.6 | 70.9 | 2109 | US-09-248-796A-2999 | Sequence 2999, App |
| 27 | 15.6 | 70.9 | 2394 | US-09-540-236-893 | Sequence 893, App |

| | | | | | |
|----|------|------|-------|---------------------|--------------------|
| 28 | 15.6 | 70.9 | 3069 | US-08-335-865J-7 | Sequence 7, Appl |
| 29 | 15.6 | 70.9 | 3805 | US-09-513-729B-10 | Sequence 10, Appl |
| 30 | 15.6 | 70.9 | 3805 | US-09-023-655-1443 | Sequence 1443, App |
| 31 | 15.6 | 70.9 | 4071 | US-09-513-057C-5 | Sequence 5, Appl |
| 32 | 15.6 | 70.9 | 4071 | US-09-746-801A-5 | Sequence 5, Appl |
| 33 | 15.6 | 70.9 | 4285 | US-09-949-016-689 | Sequence 689, App |
| 34 | 15.6 | 70.9 | 4308 | US-09-394-142B-23 | Sequence 23, Appl |
| 35 | 15.6 | 70.9 | 4643 | US-08-605-106-6 | Sequence 6, Appl |
| 36 | 15.6 | 70.9 | 5061 | US-09-355-160D-1 | Sequence 1, Appl |
| 37 | 15.6 | 70.9 | 5061 | US-10-092-219-1 | Sequence 1, Appl |
| 38 | 15.6 | 70.9 | 5296 | US-09-949-016-2362 | Sequence 2362, App |
| 39 | 15.6 | 70.9 | 8302 | US-09-234-827B-1 | Sequence 1, Appl |
| 40 | 15.6 | 70.9 | 10204 | US-09-949-016-11104 | Sequence 11104, A |
| 41 | 15.6 | 70.9 | 10482 | US-09-322-478-23 | Sequence 23, Appl |
| 42 | 15.6 | 70.9 | 10482 | US-09-586-106D-23 | Sequence 23, Appl |
| 43 | 15.6 | 70.9 | 14066 | US-09-601-198-56 | Sequence 56, Appl |
| 44 | 15.6 | 70.9 | 26709 | US-09-949-016-17520 | Sequence 17520, A |
| 45 | 15.6 | 70.9 | 34279 | US-09-596-002-26 | Sequence 26, Appl |

ALIGNMENTS

```

RESULT 1
US-09-313-294A-108
; Sequence 108, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Ialigudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PU-0017 US
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 108
; LENGTH: 133
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700548545H1
; NAME/KEY: unsure
; LOCATION: 8
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-108

Query Match      78.2% Score 17.2; DB 4; Length 133;
Best Local Similarity 86.4%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1 TCgcgttttcgtcgttttt 22
Db      72 TCgcgttttcgtcgttttt 93

RESULT 2
US-09-107-532A-292/C
; Sequence 292, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FACIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA

```

```

1      ZIP: 02354
2      COMPUTER READABLE FORM:
3      MEDIUM TYPE: CD/ROM ISO9660
4      COMPUTER: PC
5      OPERATING SYSTEM: <Unknown>
6      SOFTWARE: ASCII
7      CURRENT APPLICATION DATA:
8      APPLICATION NUMBER: US/09/107,532A
9      FILING DATE: 30-Jun-1998
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: 60/085,598
12     FILING DATE: 14 MAY 1998
13     APPLICATION NUMBER: 60/051571
14     FILING DATE: July 2, 1997
15     ATTORNEY/AGENT INFORMATION:
16     NAME: Ariandello, Pamela Deneke
17     REGISTRATION NUMBER: 40,489
18     REFERENCE/DOCKET NUMBER: GTC-012
19     TELECOMMUNICATION INFORMATION:
20     TELEPHONE: (781)893-5007
21     TELEFAX: (781)893-8277
22     INFORMATION FOR SEQ ID NO: 292:
23     SEQUENCE CHARACTERISTICS:
24         LENGTH: 513 base pairs
25         TYPE: nucleic acid
26         STRANDEDNESS: double
27         TOPOLOGY: circular
28         MOLECULE TYPE: DNA (genomic)
29         HYPOTHETICAL: NO
30         ANTI-SENSE: NO
31         ORIGINAL SOURCE:
32             ORGANISM: Enterococcus faecium
33     FEATURE:
34         NAME/KEY: misc feature
35         LOCATION: (B) LOCATION 1...513
36     SEQUENCE DESCRIPTION: SEQ ID NO: 292:
37     HS-09-107-532A-292

```

| | | | | |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match | 78.2% | Score 17.2 | DB 4 | Length 513 |
| Best Local Similarity | 86.4% | Pred. No. 1.3e+02 | | |
| Matches 19 | Conservative 0 | Mismatches 3 | Indels 0 | Gaps 0 |

[illegible]

```

RESULT 3
US-09-949-016-14223/c
; Sequence 14223, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01107
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14223
; LENGTH: 36016
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14223

```

Query Match 76.4%; Score 16.8; DB 4; Length 36016;

```
Qy      3 GTCGTTTTTCGTGGCTTTT 22
        ||||| | | |||||
Db      31422 GTCGTTTTTTGTGGCTTTT 31403

Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

RESULT 4
 US-08-629-600-1/c
 : Sequence 1, Application US/08629600
 : Patent No. 5783196
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: NORIEGA, Fernando
 : APPLICANT: LEVINE, Myron M.
 : TITLE OF INVENTION: GUA MUTANTS OF SHIGELLA
 : TITLE OF INVENTION: AND VACCINES CONTAINING THE SAME
 :
 : NUMBER OF SEQUENCES: 18
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS
 : STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
 : CITY: Washington, D.C.
 :
 : STATE: D.C.
 :
 : COUNTRY: U.S.A.
 :
 : ZIP: 20037
 :
 : COMPUTER READABLE FORM:
 :
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/629,600
 : FILING DATE: 9-APR-1996
 : CLASSIFICATION: 424
 :
 : ATTORNEY/AGENT INFORMATION:
 : NAME: KIT, Gordon
 :
 : REGISTRATION NUMBER: 30,764
 : REFERENCE/DOCKET NUMBER: A-6765
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202) 293-7060
 : TELEFAX: (202) 293-7860
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 3531 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: genomic DNA
 : HYPOTHEICAL: NO
 : ANTI-SENSE: NO
 :
 : US-08-629-600-1

| | | | | |
|-----------------------|-------|-------------------|------|--------------|
| Query Match | 74.5% | Score 16.4 | DB 1 | Length 3531 |
| Best Local Similarity | 99.4% | Pred. No. 3.3e+02 | | |
| Matches | 17 | Conservative | 0 | Mismatches 1 |
| | | | | Indels 0 |
| | | | | Gaps 0 |
| QY | 5 | CGTTTTCGTCGCGTTT | 22 | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| Db | 846 | CGTTTTCGTCGCGTTT | 829 | |

```

RESULT 5
US-09-076-761-1/c
: Sequence 1, Application US/09076761
: Patent No. 6190669
:
: GENERAL INFORMATION:
:
: APPLICANT: NORIEGA, Fernando
:
: APPLICANT: SZEIN, Marcelo B.
:
: APPLICANT: LEVIN, Myron M.
:
: TITLE OF INVENTION: ATTENUATED MUTANTS OF SALMONELLA
:
: TITLE OF INVENTION: WHICH CONSTITUTIVELY EXPRESS THE
:
: TITLE OF INVENTION: V1 ANTIGEN
:
: NUMBER OF SEQUENCES: 10

```

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,761
FILING DATE: 13-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-7140
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-09-076-761-1

Query Match

Best Local Similarity 74.5%; Score 16.4; DB 3; Length 3531;
Matches 17; Conservativity 94.4%; Pred. No. 3.3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 5 CGTTTTCGTGCGTTT 22

DB 846 CGTTTTCGTGCGATT 829

RESULT 6

US-09-134-000C-3167/C

Sequence 3167, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 3167

LENGTH: 909

TYPE: DNA

ORGANISM: Enterococcus faecalis

US-09-134-000C-3167

Query Match

Best Local Similarity 73.6%; Score 16.2; DB 4; Length 909;
Matches 18; Conservativity 85.7%; Pred. No. 3.7e+02; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTTCGTTTTCGTGCGTTT 22

DB 248 CGTTCGTTTTCGTGCGTTGT 228

RESULT 7

US-09-134-000C-3285/C

Sequence 3285, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 3285

LENGTH: 2358

TYPE: DNA

ORGANISM: Enterococcus faecalis

US-09-134-000C-3285

Query Match

Best Local Similarity 73.6%; Score 16.2; DB 4; Length 2358;
Matches 18; Conservativity 85.7%; Pred. No. 4e+02; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTTCGTTTTCGTGCGTTT 22

DB 1697 CGTTCGTTTTCGTGCGTTGT 1677

RESULT 8

US-09-489-039A-560

Sequence 560, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

FILE REFERENCE: 2709 2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 560

LENGTH: 660

TYPE: DNA

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-560

Query Match

Best Local Similarity 71.8%; Score 15.8; DB 4; Length 660;
Matches 17; Conservativity 89.5%; Pred. No. 5.4e+02; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTGCTTTTCGTGCGTTT 21

DB 426 GTGCTTTTCGTGCGTTT 444

RESULT 9

US-09-543-681A-2772

Sequence 2772, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

FILE REFERENCE: 2709 1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

```
; SEQ ID NO 2772
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-2772
```

| | | | | |
|--------------------------|--------|--------------------|-----------|-------------|
| Query Match | 70.9%; | Score 15.6; | DB 4; | Length 231; |
| Best Local Similarity | 81.8%; | Pred. No. 6.1e+02; | | |
| Matches 18; Conservative | 0; | Mismatches 4; | Indels 0; | Gaps 0 |

Qy 1 TCCTCGTTTTCGTGCGTTT 22
Db 167 TCCTCGTTTTCGTGCGTTT 188

RESULT 10
US-09-543-681A-1478/c
; Sequence 1478, Application US/09543681A
; Patent No. 6804708

```

: APPLICANT: GARY BRETON
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
: TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 2709.1002-001
: CURRENT APPLICATION NUMBER: US/09/543,681A
: CURRENT FILING DATE: 2000-04-05
: PRIOR APPLICATION NUMBER: US 60/128,706
: PRIOR FILING DATE: 1999-04-09
: NUMBER OF SEQ ID NOS: 8344
: SEQ ID NO 1478
: LENGTH: 300
: TYPE: DNA
: ORGANISM: Proteus mirabilis
: US-09-543-681A-1478

```

| | | | | |
|--------------------------|---------------------------|--------------------|-----------|-------------|
| | 70.9%; | Score 15.6; | DB 4; | Length 300; |
| Query Match | | | | |
| Best Local Similarity | 81.8%; | Pred. NO. 6.2e+02; | | |
| Matches 18; Conservative | 0; | Mismatches 4; | Indels 0; | Gaps 0; |
| Oy | 1 TCGTCGTTTTTCGTCGCTTTT | 22 | | |
| Db | 208 TCGTCGTTTTTCGTCGCTTTT | 187 | | |

```

RESULT 11
US-09-513-999C-35185
; Sequence 35185, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 35185
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-513-999C-35185

```

| | | | | | |
|-----------------------|--------------|--------------------|--------|------------|--------|
| Query Match | 70.9% | Score 15.6 | DB 4 | Length 440 | |
| Best Local Similarity | 81.8% | Pred. No. 6.4e+02 | | | |
| Matches 18 | Conservative | 4 | Indels | 0 | Gaps 0 |
| Qy | 1 | TCGCGTTTTTCGCGTTTT | 22 | | |
| | | | | | |

Db 193 TTGTCCTTTT TTGCGTTT 214

```

RESULT 12
US-09-270-767-3552/c
; Sequence 3552, Application US/09270767
; Patent No. 6703481
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3552
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-3552

```

```

Query Match      70.9%; Score 15.6; DB 4; Length 599;
Best Local Similarity 81.8%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 TCGCGCTTTTCGCGCTTTT 22
          ||||| ||||| |||||
Db      568 TCGCGCGCTCGTGTGTTTT 547

```

```

RESULT 13
US-09-270-767-18834/c
: Sequence 18834, Application US/09270767
: Patent No. 6703421
: GENERAL INFORMATION:
: APPLICANT: Homburger et al.
: TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
: FILE REFERENCE: File Reference: 7326-094
: CURRENT APPLICATION NUMBER: US/09/270,767
: CURRENT FILING DATE: 1999-03-17
: NUMBER OF SEQ ID NOS: 62517
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 18834
: LENGTH: 599
: TYPE: DNA
: ORGANISM: Drosophila melanogaster
: US-09-270-767-18834

```

| | | | | |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 70.9%; | Score 15.6; | DB 4; | Length 599; |
| Best Local Similarity | 81.8%; | Pred. No. 6.5e+02; | | |
| Matches 18; | Conservative 0; | Mismatches 4; | Indels 0; | Gaps 0; |
| QY | 1 | TCGTCGTTTTCGTGCGT | TTTT | 22 |
| | | | | |
| Db | 568 | TCGTCGTCGTGTCGTG | TTTTTT | 547 |

RESULT 14
US-09-949-016-31352/c
Sequence 31352, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 18:45:43 ; Search time 578 Seconds
(without alignments)
225.856 Million cell updates/sec

Title: US-10-613-228A-1

Perfect score: 22

Sequence: 1 tcgcgttttcgcgttttc 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 22 | 100.0 | 22 | 17 | US-10-613-228A-1 |
| 2 | 22 | 100.0 | 22 | 18 | US-10-613-228A-1 |
| 3 | 20.4 | 92.7 | 618 | 18 | US-10-363-345A-34257 |
| 4 | 20.4 | 92.7 | 618 | 18 | US-10-363-345A-34258 |
| 5 | 20.4 | 92.7 | 619 | 18 | US-10-363-345A-40287 |
| 6 | 20.4 | 92.7 | 619 | 18 | US-10-363-345A-40288 |
| 7 | 20.4 | 92.7 | 761 | 18 | US-10-363-345A-2025 |
| 8 | 20.4 | 92.7 | 761 | 18 | US-10-363-345A-2026 |
| 9 | 20.4 | 92.7 | 1024 | 18 | US-10-363-345A-7203 |
| 10 | 20.4 | 92.7 | 1024 | 18 | US-10-363-345A-7204 |
| 11 | 19.4 | 88.2 | 511 | 18 | US-10-363-345A-28015 |

| | | | | | | |
|------|------|------|---------|----|----------------------|-------------------|
| c 12 | 19.4 | 88.2 | 511 | 18 | US-10-363-345A-28016 | Sequence 28016, A |
| c 13 | 19.4 | 88.2 | 523 | 18 | US-10-363-345A-35059 | Sequence 35059, A |
| c 14 | 19.4 | 88.2 | 523 | 18 | US-10-363-345A-35060 | Sequence 35060, A |
| c 15 | 19.4 | 88.2 | 524 | 18 | US-10-363-345A-40325 | Sequence 40325, A |
| c 16 | 19.4 | 88.2 | 524 | 18 | US-10-363-345A-40326 | Sequence 40326, A |
| c 17 | 19.4 | 88.2 | 610 | 18 | US-10-363-345A-23153 | Sequence 23153, A |
| c 18 | 19.4 | 88.2 | 610 | 18 | US-10-363-345A-23154 | Sequence 23154, A |
| c 19 | 19.4 | 88.2 | 838 | 18 | US-10-363-345A-32131 | Sequence 32131, A |
| c 20 | 19.4 | 88.2 | 838 | 18 | US-10-363-345A-32132 | Sequence 32132, A |
| c 21 | 19.4 | 88.2 | 839 | 18 | US-10-363-345A-1741 | Sequence 1741, Ap |
| c 22 | 19.4 | 88.2 | 839 | 18 | US-10-363-345A-1742 | Sequence 1742, Ap |
| c 23 | 19.4 | 88.2 | 885 | 18 | US-10-363-345A-18089 | Sequence 18089, A |
| c 24 | 19.4 | 88.2 | 885 | 18 | US-10-363-345A-18090 | Sequence 18090, A |
| c 25 | 19.4 | 88.2 | 1267 | 18 | US-10-363-345A-27261 | Sequence 27261, A |
| c 26 | 19.4 | 88.2 | 1267 | 18 | US-10-363-345A-27262 | Sequence 27262, A |
| c 27 | 19.4 | 88.2 | 3673778 | 16 | US-10-312-841-2 | Sequence 2, Appl |
| c 28 | 19 | 86.4 | 920 | 18 | US-10-363-345A-20285 | Sequence 20285, A |
| c 29 | 19 | 86.4 | 920 | 18 | US-10-363-345A-20286 | Sequence 20286, A |
| c 30 | 18.8 | 85.5 | 523 | 18 | US-10-363-345A-17495 | Sequence 17495, A |
| c 31 | 18.8 | 85.5 | 523 | 18 | US-10-363-345A-17496 | Sequence 17496, A |
| c 32 | 18.8 | 85.5 | 524 | 18 | US-10-363-345A-15539 | Sequence 15539, A |
| c 33 | 18.8 | 85.5 | 524 | 18 | US-10-363-345A-15540 | Sequence 15540, A |
| c 34 | 18.8 | 85.5 | 525 | 18 | US-10-363-345A-35507 | Sequence 35507, A |
| c 35 | 18.8 | 85.5 | 525 | 18 | US-10-363-345A-35508 | Sequence 35508, A |
| c 36 | 18.8 | 85.5 | 553 | 18 | US-10-363-345A-39041 | Sequence 39041, A |
| c 37 | 18.8 | 85.5 | 553 | 18 | US-10-363-345A-39042 | Sequence 39042, A |
| c 38 | 18.8 | 85.5 | 561 | 18 | US-10-363-345A-35871 | Sequence 35871, A |
| c 39 | 18.8 | 85.5 | 561 | 18 | US-10-363-345A-35872 | Sequence 35872, A |
| c 40 | 18.8 | 85.5 | 651 | 18 | US-10-363-345A-34913 | Sequence 34913, A |
| c 41 | 18.8 | 85.5 | 651 | 18 | US-10-363-345A-34914 | Sequence 34914, A |
| c 42 | 18.8 | 85.5 | 712 | 18 | US-10-363-345A-27451 | Sequence 27451, A |
| c 43 | 18.8 | 85.5 | 712 | 18 | US-10-363-345A-27452 | Sequence 27452, A |
| c 44 | 18.8 | 85.5 | 759 | 18 | US-10-363-345A-3263 | Sequence 3263, Ap |
| c 45 | 18.8 | 85.5 | 759 | 18 | US-10-363-345A-3264 | Sequence 3264, Ap |

ALIGNMENTS

RESULT 1
US-10-613-228A-1
; Sequence 1, Application US/10613228A
; Publication No. US20040092472A1
; GENERAL INFORMATION:
; APPLICANT: KRIEG, ARTHUR M
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS FOR STIMULATING IMMUNE RESPONSES
; FILE REFERENCE: C1037, 70045US00
; CURRENT APPLICATION NUMBER: US/10/613, 228A
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US 60/394,193
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligodeoxynucleotide
US-10-613-228A-1

Query Match 100.0%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. NO. 3.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TCgcgttttcgcgttttc 22
1 TCgcgttttcgcgttttc 22
RESULT 2
US-10-816-220-152
; Sequence 152, Application US/10816220

```
; Publication No. US20040235770A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Heather L
; APPLICANT: McCLUSKEY, Michael J
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID OIL-IN-WATER FORMULATIONS AND
; TITLE OF INVENTION: RELATED METHODS OF USE
; FILE REFERENCE: C1037.70039US01
; CURRENT APPLICATION NUMBER: US/10/816,220
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 60/459,920
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US 60/461,903
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 434
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-816-220-152
```

```
Query Match          100.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TCGTCGTTTTTCGTCGTTTTT 22
    |||||
Db 1 TCGTCGTTTTTCGTCGTTTTT 22
```

```
RESULT 3
US-10-363-345A-34257
; Sequence 34257, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 34257
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 34257
US-10-363-345A-34257
```

```
Query Match          92.7%; Score 20.4; DB 18; Length 618;
Best Local Similarity 95.5%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 TCGTCGTTTTTCGTCGTTTTT 22
    |||||
Db 98 TCGTCGTTTTTCGTCGTTTTT 119
```

```
RESULT 4
US-10-363-345A-34258/C
; Sequence 34258, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
```

```
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 34258
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 34258
US-10-363-345A-34258
```

```
Query Match          92.7%; Score 20.4; DB 18; Length 618;
Best Local Similarity 95.5%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 TCGTCGTTTTTCGTCGTTTTT 22
    |||||
Db 521 TCGTCGTTTTTCGTCGTTTTT 500
```

```
RESULT 5
US-10-363-345A-40287
; Sequence 40287, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40287
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 40287
US-10-363-345A-40287
```

```
Query Match          92.7%; Score 20.4; DB 18; Length 619;
Best Local Similarity 95.5%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 TCGTCGTTTTTCGTCGTTTTT 22
    |||||
Db 190 TCGTCGTTTTTCGTCGTTTTT 211
```

```
RESULT 6
US-10-363-345A-40288/C
; Sequence 40288, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40288
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Artificial Sequence
```


FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 40288
US-10-363-345A-40288

Query Match 92.7%; Score 20.4; DB 18; Length 619;
Best Local Similarity 95.5%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 430 TCGTCGTTTTTCGTCGTTTTT 409

RESULT 7
US-10-363-345A-2025
; Sequence 2025, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2025
; LENGTH: 761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-2025

Query Match 92.7%; Score 20.4; DB 18; Length 761;
Best Local Similarity 95.5%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 598 TCGTCGTTTTTCGTCGTTTTT 619

RESULT 8
US-10-363-345A-2026/c
; Sequence 2026, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2026
; LENGTH: 761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 2026
US-10-363-345A-2026

Query Match 92.7%; Score 20.4; DB 18; Length 761;
Best Local Similarity 95.5%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 164 TCGTCGTTTTTCGTCGTTTTT 143

RESULT 9
US-10-363-345A-7203
; Sequence 7203, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 7203
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-7203

Query Match 92.7%; Score 20.4; DB 18; Length 1024;
Best Local Similarity 95.5%; Pred. No. 29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 276 TCGTCGTTTTTCGTCGTTTTT 297

RESULT 10
US-10-363-345A-7204/c
; Sequence 7204, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 7204
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 7204
US-10-363-345A-7204

Query Match 92.7%; Score 20.4; DB 18; Length 1024;
Best Local Similarity 95.5%; Pred. No. 29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 749 TCGTCGTTTTTCGTCGTTTTT 728

RESULT 11
US-10-363-345A-28015
; Sequence 28015, Application US/10363345A
; Publication No. US20040234960A1

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 28015
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 28015
US-10-363-345A-28015
```

```
Query Match      88.2%; Score 19.4; DB 18; Length 511;
Best Local Similarity 95.2%; Pred. No. 72;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CGTCGTTTTCGTCGCGTTTTT 22
Db      474 CGTCGTTTTCGGCGCGTTTTT 494
```

```
RESULT 12
US-10-363-345A-28016/c
; Sequence 28016, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 28016
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 28016
US-10-363-345A-28016
```

```
Query Match      88.2%; Score 19.4; DB 18; Length 511;
Best Local Similarity 95.2%; Pred. No. 72;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CGTCGTTTTCGTCGCGTTTTT 22
Db      38 CGTCGTTTTCGGCGCGTTTTT 18
```

```
RESULT 13
US-10-363-345A-35059
; Sequence 35059, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
```

```
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35059
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 35059
US-10-363-345A-35059
```

```
Query Match      88.2%; Score 19.4; DB 18; Length 523;
Best Local Similarity 95.2%; Pred. No. 73;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CGTCGTTTTCGTCGCGTTTTT 22
Db      488 CGTCGTTTTCGTCGTTTTT 508
```

```
RESULT 14
US-10-363-345A-35060/c
; Sequence 35060, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 35060
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 35060
US-10-363-345A-35060
```

```
Query Match      88.2%; Score 19.4; DB 18; Length 523;
Best Local Similarity 95.2%; Pred. No. 73;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CGTCGTTTTCGTCGCGTTTTT 22
Db      36 CGTCGTTTTCGTCGTTTTT 16
```

```
RESULT 15
US-10-363-345A-40325
; Sequence 40325, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 40325
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 40325
US-10-363-345A-40325
```

Query Match 88.2%; Score 19.4; DB 18; Length 524;
Best Local Similarity 95.2%; Pred. No. 73;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGTCGTTTTTCGTGCGCTTTT 22
|||||
Db 399 CGTCGTTTTTCGTGCGCTTTT 419
|||||

Search completed: March 9, 2005, 21:05:42
Job time : 581 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 14:14:33 ; Search time 3888 Seconds
(without alignments)
274.181 Million cell updates/sec

Title: US-10-613-228a-1

Perfect score: 22

Sequence: 1 tcgtcgtcttcgtcgtcttc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_beg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_yi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|-------------|
| 1 | 20.4 | 92.7 | 226153 | 2 AC073704 | Mus muscu |
| 2 | 19.4 | 88.2 | 349980 | 6 AX344573 | Sequence |
| 3 | 18.8 | 85.5 | 5826 | 6 AX356381 | Sequence |
| 4 | 18.8 | 85.5 | 6130 | 6 AX251400 | Sequence |
| 5 | 18.8 | 85.5 | 6130 | 6 AX345031 | Sequence |
| 6 | 18.8 | 85.5 | 7728 | 6 AX344979 | Sequence |
| 7 | 18.8 | 85.5 | 7728 | 6 AX348500 | Sequence |
| 8 | 18.8 | 85.5 | 8951 | 6 AX345697 | Sequence |
| 9 | 18.8 | 85.5 | 13133 | 6 AX344227 | Sequence |
| 10 | 18.4 | 83.6 | 20 | 6 AX104184 | Sequence |
| 11 | 18.4 | 83.6 | 20 | 6 AX355698 | Sequence |
| 12 | 18.4 | 83.6 | 20 | 6 AX547237 | Sequence |
| 13 | 18.4 | 83.6 | 5369 | 6 CO600212 | Sequence |
| 14 | 18.4 | 83.6 | 146491 | 2 AC019950 | Drosophi |
| 15 | 18.4 | 83.6 | 182601 | 3 AC009904 | Drosophi |
| 16 | 18.4 | 83.6 | 236375 | 3 AE003708 | Drosophi |
| 17 | 18.4 | 83.6 | 310967 | 1 AE016869 | Pseudomon |
| 18 | 18 | 81.8 | 149269 | 2 BX897667 | Danio rer |
| 19 | 17.8 | 80.9 | 1527 | 5 BC056691 | Danio rer |

| | | | | | |
|----|------|------|--------|-------------|--------------------|
| 20 | 17.8 | 80.9 | 2290 | 3 AF606934 | Af606934 Spirula s |
| 21 | 17.8 | 80.9 | 2322 | 8 AY139685 | AY139685 Porphyra |
| 22 | 17.8 | 80.9 | 2381 | 6 AX3447239 | AX3447239 Sequence |
| 23 | 17.8 | 80.9 | 7195 | 6 AX277866 | AX277866 Sequence |
| 24 | 17.8 | 80.9 | 7195 | 6 AX323551 | AX323551 Sequence |
| 25 | 17.8 | 80.9 | 11622 | 6 AX345576 | AX345576 Sequence |
| 26 | 17.8 | 80.9 | 34216 | 3 U57054 | U57054 Caenorhabdi |
| 27 | 17.8 | 80.9 | 99176 | 5 BX255893 | BX255893 Zebrafish |
| 28 | 17.8 | 80.9 | 172585 | 2 CR847782 | CR847782 Danio rer |
| 29 | 17.8 | 80.9 | 215917 | 2 AC006764 | AC006764 Caenorhab |
| 30 | 17.8 | 80.9 | 252250 | 1 AP005339 | AP005339 Vibrio vu |
| 31 | 17.8 | 80.9 | 300045 | 1 AE016803 | AE016803 Vibrio vu |
| 32 | 17.8 | 80.9 | 303121 | 1 AE016766 | AE016766 Escherich |
| 33 | 17.4 | 79.1 | 4110 | 6 AX598855 | AX598855 Sequence |
| 34 | 17.4 | 79.1 | 5774 | 6 AX278031 | AX278031 Sequence |
| 35 | 17.4 | 79.1 | 5774 | 6 AX323798 | AX323798 Sequence |
| 36 | 17.4 | 79.1 | 5938 | 6 AX344811 | AX344811 Sequence |
| 37 | 17.4 | 79.1 | 6067 | 6 AX344680 | AX344680 Sequence |
| 38 | 17.4 | 79.1 | 6124 | 8 AB010408 | AB010408 Arabidops |
| 39 | 17.4 | 79.1 | 7004 | 6 AX277956 | AX277956 Sequence |
| 40 | 17.4 | 79.1 | 7004 | 6 AX323651 | AX323651 Sequence |
| 41 | 17.4 | 79.1 | 7110 | 6 CQ806871 | CQ806871 Sequence |
| 42 | 17.4 | 79.1 | 7110 | 6 AX251243 | AX251243 Sequence |
| 43 | 17.4 | 79.1 | 7110 | 6 AX251990 | AX251990 Sequence |
| 44 | 17.4 | 79.1 | 7110 | 6 AX346458 | AX346458 Sequence |
| 45 | 17.4 | 79.1 | 7110 | 6 AX349019 | AX349019 Sequence |

ALIGNMENTS

RESULT 1
AC073704
LOCUS
DEFINITION Mus musculus clone RP23-175112, WORKING DRAFT SEQUENCE, 35
unordered pieces.
AC073704
AC073704.1 GI:8810321
HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM
MUS MUSCULUS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 226153)
DOE Joint Genome Institute.
TITLE
JOURNAL
REFERENCE
AUTHORS
TITILE
JOURNAL
COMMENT

Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1804276
Center clone name: RPCR-23_175112

Summary Statistics
Consensus quality: 200795 bases at least Q40
Consensus quality: 211634 bases at least Q30
Consensus quality: 213977 bases at least Q20
Estimated insert size: 205410; agarose-ff estimation
Estimated insert size: 222753; sum-of-ctnigs estimation
Quality coverage: 7.81 in Q20 bases; agarose-ff estimation
Quality coverage: 7.2 in Q20 bases; sum-of-ctnigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 ctnigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the ctnigs are represented as

SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of diseases associated with dna repair
JOURNAL Patent: WO 0181622-A 15 01-NOV-2001;
Epigenomics AG (DE)

FEATURES
source location/Qualifiers
1..5826
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 5826;
Best Local Similarity 90.9%; Pred. No. 6.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTCGTGCGTTT 22
|||||
1332 TCGGCGTTTTCGTGCGTTT 5588

RESULT 4
LOCUS AX251400 6130 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 368 from Patent WO0168912.
ACCESSION AX251400
VERSION AX251400.1 GI:15984823
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of diseases associated with tumor suppressor genes and
JOURNAL Patent: WO 0168912-A 368 20-SEP-2001;
Epigenomics AG (DE)

FEATURES
source location/Qualifiers
1..6130
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 6130;
Best Local Similarity 90.9%; Pred. No. 6.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTCGTGCGTTT 22
|||||
1332 TCGGCGTTTTCGTGCGTTT 1353

RESULT 5
LOCUS AX345031 6130 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 102 from Patent WO0200928.
ACCESSION AX345031
VERSION AX345031.1 GI:18492917
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 0200928-A 102 03-JAN-2002;
Epigenomics AG (DE)

FEATURES
source location/Qualifiers
1..6130
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 6130;
Best Local Similarity 90.9%; Pred. No. 6.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTCGTGCGTTT 22
|||||
1332 TCGGCGTTTTCGTGCGTTT 1353

RESULT 6
LOCUS AX344979 7728 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 50 from Patent WO0200928.
ACCESSION AX344979
VERSION AX344979.1 GI:18492865
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 0200928-A 50 03-JAN-2002;
Epigenomics AG (DE)

FEATURES
source location/Qualifiers
1..7728
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 7728;
Best Local Similarity 90.9%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTCGTGCGTTT 22
|||||
2026 TCGTCGTTTTCGTGCGTTT 2047

RESULT 7
LOCUS AX348500 7728 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 8 from Patent WO0202809.
ACCESSION AX348500
VERSION AX348500.1 GI:18614535
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of behavioural disorders, neurological disorders and
JOURNAL Cancer
Patent: WO 0202809-A 8 10-JAN-2002;
Epigenomics AG (DE)

FEATURES
source location/Qualifiers
1..7728
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 7728;
Best Local Similarity 90.9%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TCGTCGTTTTTCGCGCTTTT 22
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 2026 TCGTCGTTTTTCGCTGCTTATT 2047

RESULT 8
AX345697 8951 bp DNA linear PAT 01-FEB-2002
LOCUS Sequence 768 from Patent WO0200928.
DEFINITION AX345697
ACCESSION AX345697
VERSION AX345697.1 GI:18493583
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS 1 Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 0200928-A 768 03-JAN-2002;
Epigenomics AG (DE)

FEATURES
source Location/Qualifiers
1. 8951
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 8951;
Best Local Similarity 90.9%; Pred. No. 6.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGCGCTTTT 22
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 3724 TCGCGCTTTTCGTCGCTTTT 3745

RESULT 9
AX344227 13133 bp DNA linear PAT 01-FEB-2002
LOCUS Sequence 74 from Patent WO0200926.
DEFINITION AX344227
ACCESSION AX344227
VERSION AX344227.1 GI:18492115
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS 1 Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of diseases associated with signal transduction
JOURNAL Patent: WO 0200926-A 74 03-JAN-2002;
Epigenomics AG (DE)

FEATURES
source Location/Qualifiers
1. 13133
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 6; Length 13133;
Best Local Similarity 90.9%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGCGCTTTT 22
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 8050 TCGTCGTTTTTCGCTGCTTTT 8071

RESULT 10
AX104184 20 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 376 from Patent WO0122972.
DEFINITION AX104184
ACCESSION AX104184
VERSION AX104184.1 GI:13920381
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS 1 Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 376 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)

FEATURES
source Location/Qualifiers
1. 20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 83.6%; Score 18.4; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGCGCTTT 20
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCGTCGTTTTTCGCTGCGCTT 20

RESULT 11
AX355698 20 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 726 from Patent WO0197843.
DEFINITION AX355698
ACCESSION AX355698
VERSION AX355698.1 GI:18620366
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS 1 Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL Patent: WO 0197843-A 726 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES
source Location/Qualifiers
1. 20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"

ORIGIN

Query Match 83.6%; Score 18.4; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGCGCTTT 20
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCGTCGTTTTTCGCTGCGCTT 20

RESULT 12
AX547237 20 bp DNA linear PAT 01-MAR-2003
LOCUS Sequence 376 from Patent WO02053141.
ACCESSION AX547237
VERSION AX547237.1 GI:25812381
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1 Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 376 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1. 20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
ORIGIN
Query Match 83.6%; Score 18.4; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCGTCGTTTTGTCGCTTT 20
1 TCGTCGTTTTGTCGCTTT 20
Db 1 TCGTCGTTTTGTCGCTTT 20
RESULT 13
LOCUS CQ600212 5369 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 27970 from Patent WO0171042.
ACCESSION CQ600212
VERSION CQ600212.1 GI:41655454
KEYWORDS
SOURCE Drosophila sp.
ORGANISM Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 Venter, J.C., Adams, M., Li, P.W. and Myers, E.W.
AUTHORS Detection kit, such as nucleic acid arrays, for detecting the
TITLE expression of 10,000 or more Drosophila genes and uses thereof
JOURNAL Patent: WO 0171042-A 27970 27-SEP-2001;
PE Corporation (NY) (US)
FEATURES
source
1. 5369
/organism="Drosophila sp."
/mol_type="unassigned DNA"
/db_xref="taxon:7242"
ORIGIN
Query Match 83.6%; Score 18.4; DB 6; Length 5369;
Best Local Similarity 95.0%; Pred. No. 9.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CGTCGTTTTGTCGCTTT 21
3568 CGTCGTTTTGTCGCTTT 3587
Db 3568 CGTCGTTTTGTCGCTTT 3587
RESULT 14
LOCUS AC019950 146491 bp DNA linear HTG 03-JAN-2000
DEFINITION Drosophila melanogaster. *** SEQUENCING IN PROGRESS ***.
ACCESSION AC019950
VERSION AC019950.1 GI:6664947
KEYWORDS HTG, HTGS PHASE2.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 146491)
AUTHORS Adams, M. and Venter, J.C.

TITLE Direct Submission
JOURNAL Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10211502 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
1. 146491
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
ORIGIN
Query Match 83.6%; Score 18.4; DB 2; Length 146491;
Best Local Similarity 95.0%; Pred. No. 7.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CGTCGTTTTGTCGCTTT 21
38427 CGTCGTTTTGTCGCTTT 38446
Db 38427 CGTCGTTTTGTCGCTTT 38446
RESULT 15
LOCUS AC009904 182601 bp DNA linear INV 06-SEP-2001
DEFINITION Drosophila melanogaster, chromosome 3R, region 88B-88E, BAC clone
BACR32A03, complete sequence.
ACCESSION AC009904 AC007693
VERSION AC009904.7 GI:15451478
KEYWORDS HTG.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 182601)
AUTHORS Celisner, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Rogers, Y., An, H., Baldwin, D., Banzon, K.Y., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresner, D., Farfan, D.,
Ferrera, S., Frise, E., Galle, R.F., Gary, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hoskin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Pacheb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S.,
Phouanavong, S., Piltman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svyrskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
TITLE Sequencing of Drosophila chromosome 3R, region 88E-88E
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 182601)
Celisner, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
Butenoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
Kim, E., Lee, B., Lewis, S., Li, P., Lomtan, M.A., Mazda, P.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacheb, J.M., Park, S.,
Pfeiffer, B., Poon, L., Sequera, A., Seth, H., Shit, E.,
Svyrskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
Rubin, G.M.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
COMMENT On Sep 6, 2001 this sequence version replaced gi:13122705.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: March 9, 2005, 17:17:45 ; Search time 3444 Seconds
(without alignments)
243.152 Million cell updates/sec

Title: US-10-613-228a-1

Perfect score: 22

Sequence: 1 tcgcgttttcgcgcgtttt 22

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 6847908

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hsc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| C 1 | 20.4 | 92.7 | 433 | 4 | BG428594 602494726 |
| C 2 | 19.4 | 88.2 | 957 | 9 | AG126335 Pan tlog1 |
| C 3 | 19.4 | 88.2 | 969 | 9 | AG084147 Pan tlog1 |
| C 4 | 19.4 | 86.4 | 473 | 7 | CN197708 TGESTzy15 |
| C 5 | 18.8 | 85.5 | 698 | 1 | AV895065 |
| C 6 | 18.8 | 85.5 | 750 | 9 | CL653482 PRI0118C |
| C 7 | 18.8 | 85.5 | 755 | 5 | BP006348 BP006348 |
| C 8 | 18.8 | 85.5 | 793 | 9 | CL659802 PRI0135b |
| C 9 | 18.8 | 85.5 | 1173 | 3 | CG745933 P039-1-A0 |
| C 10 | 18.8 | 85.5 | 1201 | 3 | CG704325 Tetradon |
| C 11 | 18.8 | 85.5 | 1372 | 9 | CG751386 P045-4-D0 |
| C 12 | 18.4 | 83.6 | 506 | 2 | AV955361 AV955361 |
| C 13 | 18.4 | 83.6 | 517 | 2 | AV967757 AV967757 |
| C 14 | 18.4 | 83.6 | 651 | 5 | BM207212 BM207212 |
| C 15 | 18.4 | 83.6 | 652 | 5 | BM336085 BM336085 |
| C 16 | 18.4 | 83.6 | 661 | 5 | BM362385 BM362385 |
| C 17 | 18.4 | 83.6 | 701 | 5 | BP003979 BP003979 |
| C 18 | 18.4 | 83.6 | 706 | 5 | BM477298 BM477298 |
| C 19 | 18.4 | 83.6 | 711 | 5 | BM435032 BM435032 |
| C 20 | 18.4 | 83.6 | 1101 | 9 | CNS001Y0 |
| C 21 | 18.4 | 83.6 | 236 | 7 | W66251 |
| C 22 | 17.8 | 80.9 | 246 | 6 | CB365542 ZF001-P00 |
| C 23 | 17.8 | 80.9 | 285 | 7 | CN198693 TGESTzy16 |
| C 24 | 17.8 | 80.9 | 342 | 6 | CB353501 ZF001-P00 |

| | | | | | |
|------|------|------|-----|---|----------|
| C 25 | 17.8 | 80.9 | 362 | 1 | AV678562 |
| C 26 | 17.8 | 80.9 | 374 | 1 | AV679629 |
| C 27 | 17.8 | 80.9 | 376 | 5 | BM103452 |
| C 28 | 17.8 | 80.9 | 378 | 1 | AV894777 |
| C 29 | 17.8 | 80.9 | 396 | 6 | CB352916 |
| C 30 | 17.8 | 80.9 | 444 | 5 | BM589623 |
| C 31 | 17.8 | 80.9 | 471 | 1 | AV679587 |
| C 32 | 17.8 | 80.9 | 498 | 5 | BM575333 |
| C 33 | 17.8 | 80.9 | 498 | 7 | CN769410 |
| C 34 | 17.8 | 80.9 | 499 | 1 | AV887894 |
| C 35 | 17.8 | 80.9 | 504 | 2 | AM422790 |
| C 36 | 17.8 | 80.9 | 512 | 4 | BG892389 |
| C 37 | 17.8 | 80.9 | 513 | 7 | CN769717 |
| C 38 | 17.8 | 80.9 | 525 | 1 | AV885063 |
| C 39 | 17.8 | 80.9 | 541 | 4 | BG307575 |
| C 40 | 17.8 | 80.9 | 544 | 5 | BM104367 |
| C 41 | 17.8 | 80.9 | 545 | 5 | BM187581 |
| C 42 | 17.8 | 80.9 | 555 | 5 | BQ420126 |
| C 43 | 17.8 | 80.9 | 559 | 6 | CB353813 |
| C 44 | 17.8 | 80.9 | 563 | 4 | BI706183 |
| C 45 | 17.8 | 80.9 | 564 | 2 | BE200845 |

ALIGNMENTS

RESULT 1
BG428594/c 433 bp mRNA linear EST 14-MAR-2001

LOCUS 602494726P1 NIH_MGC_75 Homo sapiens CDNA clone IMAGE:4608342 5',
DEFINITION mRNA sequence.

ACCESSION BG428594.1 GI:13335100

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Caracanthi; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

http://image.llnl.gov

Plate: L1CM1350 row: d column: 07

High quality sequence stop: 132.

Location/Qualifiers

1. 433

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4608342"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_75"

/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_1:

SfiI (ggccgctcggcc); Site_2: SfiI (ggccctatggcc); 5' and

3' adaptor were used in cloning as follows: 5' adaptor

sequence: 5'-CACGCGCATATGCGC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGGAGCGCGGACATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.65

kb (range 0.5-4.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH_MGC Library."

ORIGIN

| | | | | | |
|------------|---|-------------|--------------------|-----------|-----------------|
| | Query Match | 92.7%; | Score 20.4; | DB 4; | Length 433; |
| | Best Local Similarity | 95.5%; | Pred. No. 1e+02; | | |
| | Matches 21; Conservative | 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| Oy | 1 TCGTCGTTTTTCGTGCGCTTTT 22 | | | | |
| Db | 390 TCGTCGCTTTTCGTGCGCTTTT 369 | | | | |
| RESULT 2 | AG126335/c | | | | |
| LOCUS | AG126335 | 957 bp | DNA | linear | GSS 04-NOV-2001 |
| DEFINITION | Pan troglodytes DNA, clone: PTB-136N20.F, genomic survey sequence. | | | | |
| ACCESSION | AG126335 | | | | |
| VERSION | AG126335.1 | GI:16655500 | | | |
| KEYWORDS | Pan troglodytes (chimpanzee) | | | | |
| SOURCE | Pan troglodytes | | | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan. | | | | |
| REFERENCE | Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Tokoki,Y., Matanabe,H. and Sakaki,Y. BAC end sequences of library PTB | | | | |
| TITLE | Unpublished | | | | |
| JOURNAL | 2 (bases 1 to 957) Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Tokoki,Y., Matanabe,H. and Sakaki,Y. Direct Submission Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan 1-7-22 Suohiro-chou,Isumura-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimbee@sc.riken.go.jp, URL:http://ngp.gsc.riken.go.jp//, Tel.:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the Red process and may have higher chance of clone tracking errors. | | | | |
| COMMENT | PRIMERS Sequencing: -21M13 LIBRARY Vector : pKS145 R.Site 1 : SacI R.Site 2 : Sact. Location/Qualifiers 1..957 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" /clone="PTB-136N20.F" /sex="male" /cell_type="lymphoblast" /clone_lib="PTB Chimpanzee Male BAC Library" | | | | |
| FEATURES | source | | | | |
| ORIGIN | | | | | |
| Oy | Query Match | 88.2%; | Score 19.4; | DB 9; | Length 957; |
| Db | Best Local Similarity | 95.2%; | Pred. No. 2.8e+02; | | |
| | Matches 20; Conservative | 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| Oy | 1 TCGTCGTTTTTCGTGCGCTTTT 21 | | | | |
| Db | 795 TCGTCGTTTTTCGTGCGCTTTT 775 | | | | |
| RESULT 3 | AG084147 | 969 bp | DNA | linear | GSS 03-NOV-2001 |
| LOCUS | AG084147 | | | | |
| DEFINITION | Pan troglodytes DNA, clone: PTB-081W22.F, genomic survey sequence. | | | | |
| ACCESSION | AG084147 | | | | |
| VERSION | AG084147.1 | GI:16635949 | | | |
| KEYWORDS | GSS. | | | | |
| SOURCE | Pan troglodytes (chimpanzee) | | | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
TITLE totoki, Y., Watanabe, H. and Sakaki, Y.
REFERENCE BAC end sequences of Library PTB
AUTHORS Unpublished
TITLE 2 (bases 1 to 969)
JOURNAL Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
TITLE totoki, Y., Watanabe, H. and Sakaki, Y.
JOURNAL Direct Submission
TITLE Submitted (02-AUG-2001) Aeo Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenho-cho, Tsukuba, Ibaraki, Japan, 305-8565, Japan
(E-mail: chimpbes@gsc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. 969
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-081M2.F"
/sex="male"
/cell_type="lymphoblast"
/clone_id="PTB Chimpanzee Male BAC library"

Query Match 88.2%; Score 19.4; DB 9; Length 969;
Best Local Similarity 95.2%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORIGIN
2 CGTCGTTTTCGTCGCTTTT 22
|||||
714 CGTCGTTTTCGTCGCTTTT 754

RESULT 4
LOCUS CN197708 473 bp mRNA linear EST 05-APR-2004
DEFINITION TgSTzyl15a11.y1 TgVEG18 Tachyzoite cDNA library-2 Toxoplasma
gondii cDNA clone TgSTzyl15a11.y1 5', mRNA sequence.
ACCESSION CN197708
VERSION CN197708.1 GI:46222647
KEYWORDS EST.
SOURCE Toxoplasma gondii
ORGANISM Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
1 (bases 1 to 473)
Tang, K., Cole, R., Fogarty, S., Sibley, L. D., Ajioke, J. A., White, M.,
Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,
Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,
Ritter, E., Bennett, J., Franklin, C., Tsagarelis, V., Ronko, I.,
Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
Toxoplasma EST Project
Unpublished (2001)
Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxowatson.wustl.edu
Contact David Sibley (toxoes@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.

Seq primer: -40UP from Glibco
High quality sequence stop: 473.
Location/Qualifiers
1. 473

/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
/clone="TGSTZY155a1.y1"
/dev_stage="Tachyzoite"
/lab_host="GC10"
/clone_lib="TVEG118 Tachyzoite cDNA library-2"
/note="Vector: pBluescript SK, Site 1: EcoRI, Site 2: XhoI. The library was constructed by Kelang Tang, Robert Cole and L. David Sibley at Washington University. cDNAs were synthesized from poly(A)+ RNasy oligo d(T) priming, size-selected and directionally cloned into the Uni-ZAP XR lambda vector (Stratagene). The primary library was mass excised as phagemids and rescued in SOLR cells. The plasmid library was recovered from the SOLR cells and transformed in mass into GC10 cells for sequencing.
WARNING: the library may contain a small percentage contaminants from human fibroblast cells."

ORIGIN

Query Match 86.4%; Score 19; DB 7; Length 473;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GTCGTTTTCGTGGCTTT 21
|||||
Db 153 GTCGTTTTCGTGGCTTT 171

RESULT 5
AV895065/c 698 bp mRNA linear EST 09-NOV-2001
DEFINITION AV895065 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone rc1ad40014 3', mRNA sequence.
ACCESSION AV895065
VERSION AV895065.1 GI:16884161
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE 1 (bases 1 to 698)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satou@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. 698

FEATURES
SOURCE
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rc1ad40014"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"

ORIGIN

Query Match 85.5%; Score 18.8; DB 1; Length 698;
Best Local Similarity 90.9%; Pred. No. 5.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTCGTGGCTTTT 22
|||||
Db 484 TCGTCGTTTTCGTGGCTTTT 463

RESULT 6
Cl653482 750 bp DNA linear GSS 09-JUL-2004
LOCUS PR10118c.G01 - PR10118c.B21 (750) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
DEFINITION Cl653482
ACCESSION Cl653482.1 GI:50132352
VERSION GSS.
KEYWORDS Pristionchus pacificus
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 750)
Srinivasan, J., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R. J.
Apparad: an Acedb database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
JOURNAL Contact: Sommer RJ
COMMENT Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
SOURCE
Location/Qualifiers
1. 750
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pBpifos-5 Fosmid vector"

ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 750;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTCGTGGCTTTT 22
|||||
Db 457 TCGTCGTTTTCGTGGCTTTT 478

RESULT 7
BP006348 755 bp mRNA linear EST 15-MAR-2002
LOCUS BP006348 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone cladd0014 5', mRNA sequence.
DEFINITION BP006348
ACCESSION BP006348.1 GI:19497825
VERSION EST.
KEYWORDS Ciona intestinalis
SOURCE Ciona intestinalis
ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE 1 (bases 1 to 755)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University

ORIGIN

Query Match 85.5%; Score 18.8; DB 1; Length 750;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: sacho@ascidian.zool.kyoto-u.ac.jp.

FEATURES

source

Location/Qualifiers
1..755

/organism="Clona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="clad40014"
/issue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"

ORIGIN

Query Match 85.5%; Score 18.8; DB 5; Length 755;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 TCGTCGTTTTCGTGCGTTT 22
|||||
Db 277 TCGTCGTTTTCGTGCGTTT 298

RESULT 8 793 bp DNA linear GSS 09-JUL-2004
CL659802 PRI0135D_D02 - PRI0135B.B21 (793) Mixed stage fosmid library of P.
LOCUS pacificus var. California Pristionchus pacificus genomic, genomic
DEFINITION survey sequence.
CL659802
CL659802.1 GI:50144272
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 793)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: Fosmid ends.

SOURCE

Location/Qualifiers
1..793

/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pBf1fos-5 Fosmid vector"

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: Fosmid ends.

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: Fosmid ends.

FEATURES

source

Location/Qualifiers
1..793

/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pBf1fos-5 Fosmid vector"

ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 793;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 TCGTCGTTTTCGTGCGTTT 22
|||||
Db 466 TCGTCGTTTTCGTGCGTTT 487

RESULT 9 1173 bp DNA linear GSS 24-OCT-2003
CG745933/c P039-1-A09.za Ppa EcORI BAC library Pristionchus pacificus genomic,
LOCUS genomic survey sequence.
DEFINITION
CG745933
CG745933.1 GI:37966859
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1173)
Srinivasan,J., Sinz,W., Jesse,T., Wigers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
22835951
12884007
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

ORGANISM

Location/Qualifiers
1..1173

/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcORI BAC library"
/note="The library was generated by a partial digest of
the genomic DNA with EcORI and cloning into the BAC
vector."

REFERENCE

AUTHORS

TITLE

Query Match 85.5%; Score 18.8; DB 9; Length 1173;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 TCGTCGTTTTCGTGCGTTT 22
|||||
Db 164 TCGTCGTTTTCGTGCGTTT 143

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES

source

Location/Qualifiers
1..1173

/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcORI BAC library"
/note="The library was generated by a partial digest of
the genomic DNA with EcORI and cloning into the BAC
vector."

ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 1173;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 TCGTCGTTTTCGTGCGTTT 22
|||||
Db 164 TCGTCGTTTTCGTGCGTTT 143

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

ORGANISM

Location/Qualifiers
1..1173

/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcORI BAC library"
/note="The library was generated by a partial digest of
the genomic DNA with EcORI and cloning into the BAC
vector."

REFERENCE

AUTHORS

TITLE

Query Match 85.5%; Score 18.8; DB 9; Length 1173;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 TCGTCGTTTTCGTGCGTTT 22
|||||
Db 164 TCGTCGTTTTCGTGCGTTT 143

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES

Location/Qualifiers
1..1173

/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcORI BAC library"
/note="The library was generated by a partial digest of
the genomic DNA with EcORI and cloning into the BAC
vector."

source
1. .1201
/organism="Tetracodon nigroviridis"
/mol_type="mRNA"
/db_xref="taxon:99883"
/tissue_type="Eyes"

ORIGIN
Query Match 85.5%; Score 18.8; DB 3; Length 1201;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTCGTTTTT 22
|||||
Db 558 TCGTCGTTTTTCGTCGTTTTT 579

RESULT 11
CG751386 1372 bp DNA linear GSS 24-OCT-2003
LOCUS P045-4-D09.yb Ppa EcORI BAC library Pristionchus pacificus genomic.
DEFINITION genomic survey sequence.
ACCESSION CG751386
VERSION CG751386.1 GI:37973790
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1372)
AUTHORS Striavaan,V., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE An integrated physical and genetic map of the nematode Pristionchus
JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE 22835951
PUBMED 12884007
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends
Location/Qualifiers
1. .1372
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_id="Ppa EcORI BAC library"
/note="The library was generated by a partial digest of
the genomic DNA with EcORI and cloning into the BAC
vector."

ORIGIN
Query Match 85.5%; Score 18.8; DB 9; Length 1372;
Best Local Similarity 90.9%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTCGTTTTT 22
|||||
Db 468 TCGTCGTTTTTCGTCGTTTTT 447

RESULT 12
AV955361/c 506 bp mRNA linear EST 14-MAR-2002
LOCUS AV955361 Nori Satoh unpublished cDNA library, egg cDNA
DEFINITION intestinal cDNA clone cleg08a22 5', mRNA sequence.
ACCESSION AV955361
VERSION AV955361.1 GI:19443660
KEYWORDS EST.

SOURCE
Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 506)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .506
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cleg08a22"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_id="Nori Satoh unpublished cDNA library, egg"

ORIGIN
Query Match 83.6%; Score 18.4; DB 2; Length 506;
Best Local Similarity 95.0%; Pred. No. 7.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTCGTTTTT 20
|||||
Db 125 TCGTCGTTTTTCGTCGTTTTT 106

RESULT 13
AV967757/c 517 bp mRNA linear EST 14-MAR-2002
LOCUS AV967757 Nori Satoh unpublished cDNA library, egg cDNA
DEFINITION intestinal cDNA clone cleg23e07 5', mRNA sequence.
ACCESSION AV967757
VERSION AV967757.1 GI:19457453
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 517)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .517
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cleg23e07"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_id="Nori Satoh unpublished cDNA library, egg"

ORIGIN
Query Match 83.6%; Score 18.4; DB 2; Length 517;
Best Local Similarity 95.0%; Pred. No. 7.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTGCGTTT 20
 Db 117 TCGTCGTCCTTTCGTGCGTTT 98

RESULT 14

LOCUS BM207212/c 651 bp mRNA linear EST 05-NOV-2002
 DEFINITION BM207212 Nori Satoh unpublished cDNA library, cleaving embryo Ciona
 intestinalis cDNA clone cici097a05 5', mRNA sequence.

ACCESSION BM207212
 VERSION BM207212.1 GI:24621826
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis

REFERENCE 1 TCGTCGTTTTTCGTGCGTTT 20
 AUTHORS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 TITLE Phlebobranchia; Clonidae; Ciona.
 JOURNAL 1 (bases 1 to 651)
 COMMENT Sato, Y., Shin-I, T., Kohara, Y. and Satoh, N.
 Unpublished (2002)
 Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: sato@ascidian.zool.kyoto-u.ac.jp.

FEATURES
 source 1.651
 location/Qualifiers
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="cici097a05"
 /tissue_type="whole body"
 /dev_stage="cleaving embryo"
 /clone_lib="Nori Satoh unpublished cDNA library, cleaving
 embryo"

ORIGIN

Query Match 83.6%; Score 18.4; DB 5; Length 651;
 Best Local Similarity 95.0%; Pred. No. 7.8e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTGCGTTT 20
 Db 612 TCGTCGTCCTTTCGTGCGTTT 593

RESULT 15
 LOCUS BM336085/c 652 bp mRNA linear EST 27-MAY-2004
 DEFINITION BM336085 Yutaka Satou unpublished cDNA library, embryo whole animal
 Ciona intestinalis cDNA clone ciem801o19 5', mRNA sequence.

ACCESSION BM336085
 VERSION BM336085.1 GI:47747886
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis

REFERENCE 1 TCGTCGTTTTTCGTGCGTTT 20
 AUTHORS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 TITLE Phlebobranchia; Clonidae; Ciona.
 JOURNAL 1 (bases 1 to 652)
 COMMENT Sato, Y., Shin-I, T., Kohara, Y. and Satoh, N.
 Unpublished (2004)
 Contact: Yutaka Satou
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4095
 Fax: 81-75-705-1113
 Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES

location/Qualifiers

source 1.652
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="ciem801o19"
 /tissue_type="whole animal"
 /dev_stage="embryo"
 /clone_lib="Yutaka Satou unpublished cDNA library, embryo
 whole animal"

ORIGIN

Query Match 83.6%; Score 18.4; DB 5; Length 652;
 Best Local Similarity 95.0%; Pred. No. 7.8e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTGCGTTT 20
 Db 406 TCGTCGTCCTTTCGTGCGTTT 387

Search completed: March 9, 2005, 19:45:52
 Job time : 3450 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 14:06:53 ; Search time 535 Seconds
(without alignments)
243.429 Million cell updates/sec

Title: US-10-613-228a-1

Perfect score: 22

Sequence: 1 tcgcgttttcgcgttccttt 22

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N Geneseq 16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 22 | 100.0 | 22 | 12 | AD116210 |
| 2 | 22 | 100.0 | 22 | 12 | ADK19243 |
| 3 | 22 | 100.0 | 22 | 12 | AD044307 |
| 4 | 20.4 | 92.7 | 618 | 6 | ABQ47667 |
| 5 | 20.4 | 92.7 | 618 | 6 | ABQ47666 |
| 6 | 20.4 | 92.7 | 619 | 6 | ABQ53697 |
| 7 | 20.4 | 92.7 | 619 | 6 | ABQ53696 |
| 8 | 20.4 | 92.7 | 761 | 6 | ABQ15435 |
| 9 | 20.4 | 92.7 | 761 | 6 | ABQ15434 |
| 10 | 20.4 | 92.7 | 1024 | 6 | ABQ20612 |
| 11 | 20.4 | 92.7 | 1024 | 6 | ABQ20613 |
| 12 | 19.4 | 88.2 | 511 | 6 | ABQ41425 |
| 13 | 19.4 | 88.2 | 511 | 6 | ABQ41424 |
| 14 | 19.4 | 88.2 | 523 | 6 | ABQ48469 |
| 15 | 19.4 | 88.2 | 523 | 6 | ABQ48468 |
| 16 | 19.4 | 88.2 | 524 | 6 | ABQ53734 |
| 17 | 19.4 | 88.2 | 524 | 6 | ABQ53735 |
| 18 | 19.4 | 88.2 | 610 | 6 | ABQ36562 |
| 19 | 19.4 | 88.2 | 610 | 6 | ABQ36563 |
| 20 | 19.4 | 88.2 | 838 | 6 | ABQ45540 |

| | | | | | | | |
|---|----|------|------|------|----|----------|--------------------|
| C | 21 | 19.4 | 88.2 | 838 | 6 | ABQ45541 | Abq45541 Oligonuc1 |
| C | 22 | 19.4 | 88.2 | 839 | 6 | ABQ15151 | Abq15151 Oligonuc1 |
| C | 23 | 19.4 | 88.2 | 839 | 6 | ABQ15150 | Abq15150 Oligonuc1 |
| C | 24 | 19.4 | 88.2 | 885 | 6 | ABQ31498 | Abq31498 Oligonuc1 |
| C | 25 | 19.4 | 88.2 | 885 | 6 | ABQ31499 | Abq31499 Oligonuc1 |
| C | 26 | 19.4 | 88.2 | 1267 | 6 | ABQ40670 | Abq40670 Oligonuc1 |
| C | 27 | 19.4 | 88.2 | 1267 | 6 | ABQ40671 | Abq40671 Oligonuc1 |
| C | 28 | 19.4 | 86.4 | 23 | 12 | ADK19257 | Adk19257 Immunosti |
| C | 29 | 19.4 | 86.4 | 23 | 12 | ADK19276 | Adk19276 Immunosti |
| C | 30 | 19.4 | 86.4 | 920 | 6 | ABQ33695 | Abq33695 Oligonuc1 |
| C | 31 | 19.4 | 86.4 | 920 | 6 | ABQ33694 | Abq33694 Oligonuc1 |
| C | 32 | 18.8 | 85.5 | 523 | 6 | ABQ30904 | Abq30904 Oligonuc1 |
| C | 33 | 18.8 | 85.5 | 523 | 6 | ABQ30905 | Abq30905 Oligonuc1 |
| C | 34 | 18.8 | 85.5 | 524 | 6 | ABQ29009 | Abq29009 Oligonuc1 |
| C | 35 | 18.8 | 85.5 | 524 | 6 | ABQ29008 | Abq29008 Oligonuc1 |
| C | 36 | 18.8 | 85.5 | 525 | 6 | ABQ48916 | Abq48916 Oligonuc1 |
| C | 37 | 18.8 | 85.5 | 525 | 6 | ABQ48917 | Abq48917 Oligonuc1 |
| C | 38 | 18.8 | 85.5 | 553 | 6 | ABQ52450 | Abq52450 Oligonuc1 |
| C | 39 | 18.8 | 85.5 | 553 | 6 | ABQ52451 | Abq52451 Oligonuc1 |
| C | 40 | 18.8 | 85.5 | 561 | 6 | ABQ49381 | Abq49381 Oligonuc1 |
| C | 41 | 18.8 | 85.5 | 561 | 6 | ABQ49380 | Abq49380 Oligonuc1 |
| C | 42 | 18.8 | 85.5 | 651 | 6 | ABQ48323 | Abq48323 Oligonuc1 |
| C | 43 | 18.8 | 85.5 | 651 | 6 | ABQ48322 | Abq48322 Oligonuc1 |
| C | 44 | 18.8 | 85.5 | 712 | 6 | ABQ40860 | Abq40860 Oligonuc1 |
| C | 45 | 18.8 | 85.5 | 712 | 6 | ABQ40861 | Abq40861 Oligonuc1 |

ALIGNMENTS

RESULT 1
AD116210
ID AD116210 standard; DNA, 22 BP.
XX
XX
AC AD116210;
XX
XX
DT 22-APR-2004 (first entry)
XX
XX
DE Immunostimulatory oligodeoxynucleotide ODN 10106 SEQ ID NO:141.
XX
XX
KW ds; immunostimulatory; antibacterial; antiallergic; antiasthmatic;
KW cytosolic; virucide; fungicide; antiparasitic; interleukin antagonist;
KW gene therapy; infectious disease; allergy; asthma; cancer.
XX
XX
OS Unidentified.
XX
XX
PN WO2004005476-A2.
XX
XX
PD 15-JAN-2004.
XX
XX
PF 03-JUL-2003; 2003WO-US021113.
XX
XX
PR 03-JUL-2002; 2002US-0393880P.
PR 03-JUL-2002; 2002US-0394090P.
PR 03-JUL-2002; 2002US-0394091P.
PR 03-JUL-2002; 2002US-0394164P.
PR 03-JUL-2002; 2002US-0394193P.
PA (COLE-) COLEY PHARM GROUP INC.
XX
XX
PI Krieger AM;
XX
XX
DR WPI; 2004-091353/09.
XX
XX
PT New immunostimulatory nucleic acid molecule composition comprising CpG
PT motifs, useful for diagnosing, preventing and/or treating infectious
PT diseases, allergies, asthma and cancers.
XX
XX
PS Claim 1; SEQ ID NO 141; 257bp; English.
XX
XX
CC The invention relates to a novel composition comprising an
CC immunostimulatory nucleic acid molecule. A composition of the invention
CC has antibacterial, antiallergic, antiasthmatic, cytostatic, virucide,

CC fungicide, and antiparasitic activity. A composition may act as an
CC interleukin antagonist-4, or interleukin antagonist-5, and may have a use
CC in gene therapy. The methods and compositions of the present invention
CC are useful for diagnosing, preventing and/or treating infectious disease,
CC allergy, asthma, cancer, where the infectious disease is a herpes simplex
CC virus, bacterial, fungal or parasitic infection, and where the cancer is
CC a biliary tract cancer, bone cancer, brain and CNS cancer, breast cancer,
CC cervical cancer, choriocarcinoma, colon cancer, connective tissue cancer,
CC endometrial cancer, esophageal cancer, eye cancer, gastric cancer,
CC Hodgkin's lymphoma, interepithelial neoplasms, larynx cancer, lymphomas,
CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC neuroblastoma, oral cavity cancer, ovarian cancer, pancreas cancer,
CC prostate cancer, rectal cancer, sarcoma, skin cancer, testicular cancer,
CC thyroid cancer and renal cancer. The present sequence represents an
CC immunostimulatory nucleic acid molecule of the invention.
SQ Sequence 22 BP; 0 A; 4 C; 5 G; 13 T; 0 U; 0 Other;
Query Match 100.0%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTCGTTTTTCGTGCGTTTTT 22
DB 1 TCGTCGTTTTTCGTGCGTTTTT 22
RESULT 2
ADK19243
ID ADK19243 standard; DNA; 22 BP.
AC ADK19243;
XX
XX
DT 20-MAY-2004 (first entry)
XX
XX
DE Immunostimulatory nucleic acid #289.
XX
XX
KW Immunostimulatory nucleic acid; asthma; allergy; cancer;
KW infectious disease; autoimmune disease; airway remodeling;
KW chronic obstructive pulmonary disease; asthma; IL-6; interleukin-6;
KW TNFalpha; tumour necrosis factor alpha; IFNalpha; interferon-alpha;
KW IFNgamma; interferon-gamma; IP-10; interferon inducible protein;
KW viral infection; bacteria infection; parasitic infection; ss.
XX
OS Synthetic.
XX
XX
PN WO2004016805-A2.
XX
XX
PD 26-FEB-2004.
XX
XX
PF 19-AUG-2003; 2003WO-US025935.
XX
XX
PR 19-AUG-2002; 2002US-0404479P.
PR 19-AUG-2002; 2002US-0404820P.
PR 27-NOV-2002; 2002US-0429701P.
PR 14-FEB-2003; 2003US-0447377P.
XX
XX
PA (COLE-) COLEY PHARM GROUP INC.
PA (COLE-) COLEY PHARM GMBH.
XX
XX
PI Krieg AM, Samulowitz U, Vollmer J, Uhlmann E, Jark M, Lipford G,
PI Rankin R;
XX
XX
DR WPI; 2004-257200/24.
XX
XX
PT New immunostimulatory nucleic acid molecule having pyrimidine-purine
PT dinucleotide and a chimeric backbone, useful in treating and preventing
PT asthma, allergy, cancer, infectious disease, autoimmune disease or airway
PT remodeling.
XX
XX
PS Example 15; SEQ ID NO 290; 276pp; English.
XX
XX
CC The invention relates to an immunostimulatory nucleic acid molecule

CC comprising an internal pyrimidine-purine (YZ) dinucleotide and chimeric
CC backbone, where one internal YZ dinucleotide has a phosphodiester(-like)
CC internucleotide linkage, where optionally each additional internal YZ
CC dinucleotide has a phosphodiester(-like) or stabilised internucleotide
CC linkage, where other internucleotide linkages are stabilised. The
CC oligonucleotide is useful in stimulating or modulating an immune
CC response. The medicament shifts the immune response to a Th1 biased
CC response from a Th2 biased response. The oligonucleotide is also useful
CC in the manufacture of a medicament for treating asthma, allergy, cancer,
CC infectious disease, autoimmune disease, airway remodeling or chronic
CC obstructive pulmonary disease or in treating a subject who is a smoker or
CC who is free of symptoms of asthma. The oligonucleotide is useful in
CC inducing cytokine expression, e.g. IL-6 (interleukin-6), TNFalpha (tumour
CC necrosis factor alpha), IFNalpha (interferon-alpha), IFNgamma (interferon
CC -gamma) and IP-10 (interferon inducible protein). The oligonucleotide is
CC also useful in treating and preventing infections caused by viruses,
CC bacteria and parasites. The present sequence represents an
CC immunostimulatory nucleic acid.
SQ Sequence 22 BP; 0 A; 4 C; 5 G; 13 T; 0 U; 0 Other;
XX
XX
Query Match 100.0%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTCGTTTTTCGTGCGTTTTT 22
DB 1 TCGTCGTTTTTCGTGCGTTTTT 22
RESULT 3
ADO44307
ID ADO44307 standard; DNA; 22 BP.
AC ADO44307;
XX
XX
DT 29-JUL-2004 (first entry)
XX
XX
DE Nucleotide sequence of a Cpg ODN of class B.
XX
XX
KW HCV infection; Cpg therapy; immunostimulatory; hepatotropic; virucide;
KW gene therapy; ss.
XX
OS Synthetic.
XX
XX
PN WO2004039829-A2.
XX
XX
PD 13-MAY-2004.
XX
XX
PF 29-OCT-2003; 2003WO-IB005520.
XX
XX
PR 29-OCT-2002; 2002US-0421987P.
XX
XX
PA (COLE-) COLEY PHARM GROUP LTD.
PA (COLE-) COLEY PHARM GMBH.
XX
XX
PI Ahluwalia NK, Eflier SM, Davis HU, Vollmer J;
XX
XX
DR WPI; 2004-376156/35.
XX
XX
PT Treating a patient having hepatitis C virus (HCV) infection that was not
PT successfully treated using a previous non-Cpg therapy comprises
PT administering to a subject a Cpg immunostimulatory nucleic acid.
XX
XX
PS Example; SEQ ID NO 6; 89pp; English.
XX
XX
CC The invention relates to creating a patient having hepatitis C virus
CC (HCV) infection that was not successfully treated using a previous non-
CC Cpg therapy. The method involves administering to a subject in need of
CC such treatment a Cpg immunostimulatory nucleic acid in an amount
CC effective to treat the infection. In the treatment method, the non-Cpg
CC therapy includes interferon-alpha. The interferon-alpha is interferon-
CC alpha-2b, interferon-alpha-2a or consensus interferon-alpha. The non-Cpg

CC therapy includes interferon-alpha or pegylated interferon-alpha and
CC ribavirin. The CpG immunostimulatory nucleic acid is A, B or C class CpG
CC immunostimulatory nucleic acid. The method further comprises
CC administering interferon-alpha to the subject. The interferon-alpha is
CC administered substantially simultaneously with the CpG immunostimulatory
CC nucleic acid. The CpG immunostimulatory nucleic acid comprises a backbone
CC modification, preferably a phosphorochonate backbone modification. The
CC CpG immunostimulatory nucleic acid comprises a semi-soft backbone. The
CC method is useful for treating a patient having hepatitis C virus (HCV)
CC infection that was not successfully treated using a previous non-CpG
CC therapy. Sequences ADO44302-ADO44317 represent examples of CpG
CC oligodeoxynucleotides (ODN) which were used in the experiments to
CC exemplify the methods of the invention.

XX Sequence 22 BP; 0 A; 4 C; 5 G; 13 T; 0 U; 0 Other;
XX SQ

Query Match 100.0%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
1 TCGTCGTTTTTCGTCGTTTTT 22
Db

RESULT 4
ABQ47667/c
ID ABQ47667 standard; DNA; 618 BP.
XX
AC ABQ47667;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34258.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
XX WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:

X

CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ1410
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention

XX Sequence 618 BP; 241 A; 204 C; 58 G; 115 T; 0 U; 0 Other;
XX SQ

Query Match 92.7%; Score 20.4; DB 6; Length 618;
Best Local Similarity 95.5%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22
521 TCGTCGTTTTTCGTCGTTTTT 500
Db

RESULT 5
ABQ47666
ID ABQ47666 standard; DNA; 618 BP.
XX
AC ABQ47666;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 34257.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
XX WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,

particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. AB013410-CC AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention

Sequence 618 BP; 115 A; 58 C; 204 G; 241 T; 0 U; 0 Other;

Query Match Best Local Similarity 92.7%; Score 20.4; DB 6; Length 618;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TCCTCGTTTTTCGTGCGTTTTT 22
|||||
98 TCCTCGTTTTTCGTGCGTTTTT 119

RESULT 6
AB053697/c

ID AB053697 standard; DNA; 619 BP.

AB053697;

12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 40288.

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens.

WO200218632-A2.

07-MAR-2002.

01-SEP-2001; 2001WO-EP010074.

01-SEP-2000; 2000DE-01043826.
05-SEP-2000; 2000DE-01044543.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K, Guetig D;

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridized to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridization to both classes is determined from the label on the amplicon. From the ratio of labels hybridized to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation

status of many C residues to be determined simultaneously. AB013410-CC AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention

Sequence 619 BP; 241 A; 205 C; 57 G; 116 T; 0 U; 0 Other;

Query Match Best Local Similarity 92.7%; Score 20.4; DB 6; Length 619;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TCCTCGTTTTTCGTGCGTTTTT 22
|||||
430 TCCTCGTTTTTCGTGCGTTTTT 409

RESULT 7
AB053696
ID AB053696 standard; DNA; 619 BP.

AB053696;

12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 40287.

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens.

WO200218632-A2.

07-MAR-2002.

01-SEP-2001; 2001WO-EP010074.

01-SEP-2000; 2000DE-01043826.
05-SEP-2000; 2000DE-01044543.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K, Guetig D;

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridized to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridization to both classes is determined from the label on the amplicon. From the ratio of labels hybridized to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. AB013410-CC AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the

CC disclosure of the invention
XX Sequence 619 BP; 116 A; 57 C; 205 G; 241 T; 0 U; 0 Other;
SQ Query Match 92.7%; Score 20.4; DB 6; Length 619;
Best Local Similarity 95.5%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 190 TCGTCGTTTTTCGTCGTTTTT 211

RESULT 8
ABQ15435/C
ID ABQ15435 standard; DNA; 761 BP.
XX
XX ABQ15435;
AC
XX
XX 12-JUN-2002 (first entry)
DT
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 2026.
DE
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
XX Homo sapiens.
OS
XX WO200218632-A2.
XX
XX 07-MAR-2002.
PD
XX
XX 01-SEP-2001; 2001WO-EP010074.
PF
XX
XX 01-SEP-2000; 2000DE-01043826.
PR
XX 05-SEP-2000; 2000DE-01044543.
XX
XX (EPIC-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K, Guectig D;
PI
XX WPI; 2002-371829/40.
DR
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ34121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
XX Sequence 761 BP; 238 A; 332 C; 100 G; 91 T; 0 U; 0 Other;

Query Match 92.7%; Score 20.4; DB 6; Length 761;
Best Local Similarity 95.5%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TCGTCGTTTTTCGTCGTTTTT 22
Db 164 TCGTCGTTTTTCGTCGTTTTT 143

RESULT 9
ABQ15434
ID ABQ15434 standard; DNA; 761 BP.
XX
XX ABQ15434;
AC
XX
XX 12-JUN-2002 (first entry)
DT
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 2025.
DE
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
XX Homo sapiens.
OS
XX WO200218632-A2.
XX
XX 07-MAR-2002.
PD
XX
XX 01-SEP-2001; 2001WO-EP010074.
PF
XX
XX 01-SEP-2000; 2000DE-01043826.
PR
XX 05-SEP-2000; 2000DE-01044543.
XX
XX (EPIC-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K, Guectig D;
PI
XX WPI; 2002-371829/40.
DR
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ34121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
XX Sequence 761 BP; 91 A; 100 C; 332 G; 238 T; 0 U; 0 Other;

Query Match 92.7%; Score 20.4; DB 6; Length 761;
Best Local Similarity 95.5%; Pred. No. 26;

XX 12-JUL-2002 (first entry)
 DT Oligonucleotide for detecting cytosine methylation SEQ ID NO 35060.
 XX
 DE Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 XX drug; side effect; cancer; central nervous system; cardiovascular;
 KM gastrointestinal; respiratory system; single nucleotide polymorphism;
 KM SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200218632-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP010074.
 XX
 PR 01-SEP-2000; 2000DE-01043826.
 PR 05-SEP-2000; 2000DE-01044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;
 PI WPI; 2002-371829/40.
 DR
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.
 PS
 XX Claim 12; 56bp + Sequence Listing; 56bp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention
 CC
 XX
 SQ Sequence 523 BP; 191 A; 207 C; 61 G; 64 T; 0 U; 0 Other;
 XX
 QY Query Match 88.2%; Score 19.4; DB 6; Length 523;
 Db Best Local Similarity 95.2%; Pred. No. 70;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 2 CGTCGTTTTCGTCGTTTTT 22
 |||||
 36 CGTCGTTTTTCGTTCTGTTTTT 16
 |||||
 RESULT 15
 ID ABQ48468
 ID ABQ48468 standard; DNA; 523 BP.
 XX
 AC ABQ48468;
 XX
 XX 12-JUL-2002 (first entry)
 XX

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 35059.
 XX
 XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KM drug; side effect; cancer; central nervous system; cardiovascular;
 KM gastrointestinal; respiratory system; single nucleotide polymorphism;
 KM SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200218632-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP010074.
 XX
 PR 01-SEP-2000; 2000DE-01043826.
 PR 05-SEP-2000; 2000DE-01044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;
 PI WPI; 2002-371829/40.
 DR
 XX
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.
 PS
 XX Claim 12; 56bp + Sequence Listing; 56bp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation
 CC status of many C residues to be determined simultaneously. ABQ13410-
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention
 CC
 XX
 SQ Sequence 523 BP; 64 A; 61 C; 207 G; 191 T; 0 U; 0 Other;
 XX
 QY Query Match 88.2%; Score 19.4; DB 6; Length 523;
 Db Best Local Similarity 95.2%; Pred. No. 70;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 2 CGTCGTTTTCGTCGTTTTT 22
 |||||
 488 CGTCGTTTTTCGTTCTGTTTTT 508
 |||||
 Search completed: March 9, 2005, 17:40:33
 Job time : 537 secs